

RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 09 840 243A

Source: OIPB

Date Processed by STIC: 10/27/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u>  | <u>SUGGESTED CORRECTION</u>  | <u>SERIAL NUMBER:</u> <u>09/940243A</u> |
|--|--|---|
| <b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P</b> |  |   |
| 1 <input type="checkbox"/> Wrapped Nucleic<br>Wrapped Aminos                                     | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."  |   |
| 2 <input type="checkbox"/> Invalid Line Length   | The rules require that a line not exceed 72 characters in length. This includes white spaces.  |   |
| 3 <input type="checkbox"/> Misaligned Amino<br>Numbering   | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  |   |
| 4 <input type="checkbox"/> Non-ASCII   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.   |   |
| 5 <input type="checkbox"/> Variable Length.  | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.   |   |
| 6 <input type="checkbox"/> PatentIn 2.0<br>"bug"   | A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.   |   |
| 7 <input type="checkbox"/> Skipped Sequences<br>(OLD RULES)                                      | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |   |
| 8 <input type="checkbox"/> Skipped Sequences<br>(NEW RULES)                                      | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence<br><210> sequence id number<br><400> sequence id number<br>000  |   |
| 9 <input checked="" type="checkbox"/> Use of n's or Xaa's<br>(NEW RULES)                         | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents  |   |
| 10 <input type="checkbox"/> Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or Artificial Sequence   |   |
| 11 <input type="checkbox"/> Use of <220>   | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.<br>Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)  |   |
| 12 <input type="checkbox"/> PatentIn 2.0<br>"bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |   |
| 13 <input type="checkbox"/> Misuse of n  | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.  |   |

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/840,243A

DATE: 10/29/2001  
TIME: 13:29:31

Input Set : A:\B3991AB\_SQL.txt  
Output Set: N:\CRF3\10292001\I840243A.raw

3 <110> APPLICANT: NOVIMMUNE SA  
 5 <120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,  
 6 SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION  
 7 FACTOR AND MEDICAL USES OF THESE SUBSTANCES  
 9 <130> FILE REFERENCE: B3991AB-CS/KR  
 11 <140> CURRENT APPLICATION NUMBER: US/09/840,243A  
 12 <141> CURRENT FILING DATE: 2001-04-24  
 14 <150> PRIOR APPLICATION NUMBER: 98120085.0  
 15 <151> PRIOR FILING DATE: 1998-10-24  
 17 <160> NUMBER OF SEQ ID NOS: 19  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 40  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
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 30 ccgtacgcgt cttagaccatg gagcttaccc agcctgcaga 40  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 31  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
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 42 ttcaattct cgagtgtctg agtcccccggc a 31  
 45 <210> SEQ ID NO: 3  
 46 <211> LENGTH: 37  
 47 <212> TYPE: DNA  
 48 <213> ORGANISM: Artificial Sequence  
 50 <220> FEATURE:  
 51 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
 53 <400> SEQUENCE: 3  
 54 ccgtacgcgt cttagaccatg gagcccaactc aggttgc 37  
 57 <210> SEQ ID NO: 4  
 58 <211> LENGTH: 32  
 59 <212> TYPE: DNA  
 60 <213> ORGANISM: Artificial Sequence  
 62 <220> FEATURE:  
 63 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
 65 <400> SEQUENCE: 4  
 66 ttcaattct cgagtgcctg ggttccagca gg  
 69 <210> SEQ ID NO: 5  
 70 <211> LENGTH: 30  
 71 <212> TYPE: DNA  
 72 <213> ORGANISM: Artificial Sequence

32 Erroneous  
check distal  
c

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/840,243A

DATE: 10/29/2001  
TIME: 13:29:31

Input Set : A:\B3991AB\_SQL.txt  
Output Set: N:\CRF3\10292001\I840243A.raw

74 <220> FEATURE:  
75 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
77 <400> SEQUENCE: 5  
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83 <212> TYPE: DNA  
84 <213> ORGANISM: Artificial Sequence  
86 <220> FEATURE:  
87 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
89 <400> SEQUENCE: 6  
90 ctttcgaatt ctgcgtcttt tgccaggatg 30  
93 <210> SEQ ID NO: 7  
94 <211> LENGTH: 30  
95 <212> TYPE: DNA  
96 <213> ORGANISM: Artificial Sequence  
98 <220> FEATURE:  
99 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
101 <400> SEQUENCE: 7  
102 gtttctctag attggcagca ctggggatag 30  
105 <210> SEQ ID NO: 8  
106 <211> LENGTH: 30  
107 <212> TYPE: DNA  
108 <213> ORGANISM: Artificial Sequence  
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111 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
113 <400> SEQUENCE: 8  
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117 <210> SEQ ID NO: 9  
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119 <212> TYPE: DNA  
120 <213> ORGANISM: Artificial Sequence  
122 <220> FEATURE:  
123 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
125 <400> SEQUENCE: 9  
126 ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct taccagcct 60  
128 gcagaagac 69  
131 <210> SEQ ID NO: 10  
132 <211> LENGTH: 1345  
133 <212> TYPE: DNA  
134 <213> ORGANISM: Homo sapiens  
136 <220> FEATURE:  
137 <221> NAME/KEY: CDS  
138 <222> LOCATION: (418)..(1200)  
140 <400> SEQUENCE: 10  
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143 gcgtggtgg a gcaacacca ggcaggagag gggaaagaac tctctccctt tctgaacccc 120  
145 ctttccttg agagacgatg tgggggagtc ctccacgcat tacccactcg gccgcacaaa 180  
147 actccctctt ttagccctct gccccggccc ttgcttataa gcctttgaga ccgcagaagg 240

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PATENT APPLICATION: US/09/840,243A

DATE: 10/29/2001  
TIME: 13:29:31

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Output Set: N:\CRF3\10292001\I840243A.raw

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |     |      |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|-----|------|-----|-----|-----|
| 149 | gac | ctt | gtt | g   | tg  | gaa | ac  | gg  | g   | ga  | gg  | cc  | ag  | at  | cg  | tc  | g   | ag  | gg  | gt  | cc | gg | t   | ct   | cc  | ca  | 300 |
| 151 | gtt | g   | c   | c   | tcc | tg  | c   | tat | a   | tcc | at  | tgg | a   | ag  | ag  | aaa | ag  | ttt | gt  | ttt | gg | cc | cc  | aa   | gt  | ttt | 360 |
| 153 | gag | aga | act | g   | g   | c   | t   | ttc | gg  | g   | gg  | gg  | gg  | ac  | ag  | ag  | gg  | gt  | gg  | gg  | ac | cc | cc  | cc   | cc  | 417 |     |
| 155 | at  | g   | g   | at  | c   | t   | cc  | acc | cag | c   | c   | t   | c   | t   | c   | at  | c   | ag  | ac  | c   | ag | c  | ag  | cc   | cc  | 465 |     |
| 156 | Met | Glu | Leu | Thr | Gln | Pro | Ala | Glu | Asp | Leu | Ile | Gln | Thr | Gln | Gln | Thr |     |     |     |     |    |    |     |      |     |     |     |
| 157 | 1   |     |     |     |     |     |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     |    |    |     |      |     | 15  |     |
| 159 | cct | g   | cc  | tca | gaa | ctt | ggg | g   | ac  | cct | gaa | gac | ccc | g   | ga  | g   | ag  | g   | ag  | g   | ct | g  | ca  | 513  |     |     |     |
| 160 | Pro | Ala | Ser | Glu | Leu | Gly | Asp | Pro | Glu | Asp | Pro | Gly | Glu | Glu | Ala | Ala |     |     |     |     |    |    |     |      |     |     |     |
| 161 |     |     |     |     |     |     |     |     |     | 20  |     |     |     |     |     |     |     | 25  |     |     |    |    |     |      |     | 30  |     |
| 163 | gat | ggc | tca | gac | act | gt  | g   | tc  | ct  | ag  | ct  | tc  | ttt | cc  | t   | g   | cc  | ac  | c   | c   | tt | gg | aa  | 561  |     |     |     |
| 164 | Asp | Gly | Ser | Asp | Thr | Val | Val | Leu | Ser | Leu | Phe | Pro | Cys | Thr | Pro | Glu |     |     |     |     |    |    |     |      |     |     |     |
| 165 |     |     |     |     |     |     |     |     |     | 35  |     |     |     |     |     |     |     | 40  |     |     |    |    |     |      |     | 45  |     |
| 167 | cct | gt  | g   | at  | c   | c   | gaa | ccg | g   | at  | gt  | t   | cc  | t   | ct  | cc  | c   | ag  | g   | ca  | gg | cc | 609 |      |     |     |     |
| 168 | Pro | Val | Asn | Pro | Glu | Pro | Asp | Ala | Ser | Val | Ser | Ser | Pro | Gln | Ala | Gly |     |     |     |     |    |    |     |      |     |     |     |
| 169 |     |     |     |     |     |     |     |     |     | 50  |     |     |     |     |     |     |     | 55  |     |     |    |    |     |      |     | 60  |     |
| 171 | agc | tcc | ct  | g   | a   | ag  | cac | tcc | ac  | act | ct  | cc  | ac  | cc  | gg  | ca  | gg  | gg  | aa  | cc  | gg | aa | cc  | 657  |     |     |     |
| 172 | Ser | Ser | Leu | Lys | His | Ser | Thr | Thr | Leu | Thr | Asn | Arg | Gln | Arg | Gly | Asn |     |     |     |     |    |    |     |      |     |     |     |
| 173 | 65  |     |     |     |     |     |     |     |     | 70  |     |     |     |     |     |     |     | 75  |     |     |    |    |     |      |     | 80  |     |
| 175 | gag | gt  | g   | tca | g   | c   | t   | ct  | gg  | cc  | ac  | ct  | g   | ac  | tcc | ct  | cc  | at  | cac | ca  | gg | cc | 705 |      |     |     |     |
| 176 | Glu | Val | Ser | Ala | Leu | Pro | Ala | Thr | Leu | Asp | Ser | Leu | Ser | Ile | His | Gln |     |     |     |     |    |    |     |      |     |     |     |
| 177 |     |     |     |     |     |     |     |     |     | 85  |     |     |     |     |     |     |     | 90  |     |     |    |    |     |      |     | 95  |     |
| 179 | ctc | g   | ca  | g   | c   | gg  | g   | ag  | ct  | g   | ac  | ct  | g   | aa  | gg  | at  | tt  | cg  | gg  | aa  | aa | tt | cg  | aa   | 753 |     |     |
| 180 | Leu | Ala | Ala | Gln | Gly | Glu | Leu | Asp | Gln | Leu | Lys | Glu | His | Leu | Arg | Lys |     |     |     |     |    |    |     |      |     |     |     |
| 181 |     |     |     |     |     |     |     |     |     | 100 |     |     |     |     |     |     |     | 105 |     |     |    |    |     |      |     | 110 |     |
| 183 | gt  | g   | a   | c   | tc  | gt  | cc  | a   | cc  | ct  | g   | ac  | tcc | ct  | cc  | at  | cac | ca  | gg  | cc  | tt | cc | cc  | 801  |     |     |     |
| 184 | Gly | Asp | Asn | Leu | Val | Asn | Lys | Pro | Asp | Glu | Arg | Gly | Phe | Thr | Pro | Leu |     |     |     |     |    |    |     |      |     |     |     |
| 185 |     |     |     |     |     |     |     |     |     | 115 |     |     |     |     |     |     |     | 120 |     |     |    |    |     |      |     | 125 |     |
| 187 | at  | c   | tgg | g   | cc  | tcc | gg  | ttt | g   | ga  | g   | at  | g   | ac  | cc  | tt  | cg  | cc  | t   | tc  | ct | ct | ct  | 849  |     |     |     |
| 188 | Ile | Trp | Ala | Ser | Ala | Phe | Gly | Glu | Ile | Gl  | u   | Th  | ra  | Val | Arg | Phe | Leu | Leu |     |     |    |    |     |      |     |     |     |
| 189 |     |     |     |     |     |     |     |     |     | 130 |     |     |     |     |     |     |     | 135 |     |     |    |    |     |      |     | 140 |     |
| 191 | gag | tgg | gg  | gt  | g   | cc  | g   | cc  | c   | ac  | at  | ct  | g   | ca  | aa  | g   | ag  | ca  | g   | ag  | ac | cc | cc  | 897  |     |     |     |
| 192 | Glu | Trp | Gly | Ala | Asp | Pro | His | Ile | Leu | Ala | Lys | Glu | Arg | Glu | Ser | Ala |     |     |     |     |    |    |     |      |     |     |     |
| 193 | 145 |     |     |     |     |     |     |     |     | 150 |     |     |     |     |     |     |     | 155 |     |     |    |    |     |      |     | 160 |     |
| 195 | ctg | tc  | g   | cc  | ag  | ca  | gg  | cc  | g   | cc  | tac | ac  | ac  | g   | at  | gt  | gg  | gg  | ct  | ct  | ct | ct | ct  | 945  |     |     |     |
| 196 | Leu | Ser | Leu | Ala | Ser | Thr | Gly | Gly | Tyr | Th  | ra  | Asp | Ile | Val | Gly | Leu | Leu |     |     |     |    |    |     |      |     |     |     |
| 197 |     |     |     |     |     |     |     |     |     | 165 |     |     |     |     |     |     |     | 170 |     |     |    |    |     |      |     | 175 |     |
| 199 | ctg | g   | ag  | cg  | gt  | g   | ac  | at  | ac  | at  | tat | g   | at  | tgg | aa  | t   | gg  | gg  | ac  | gg  | cc | tt | cc  | 993  |     |     |     |
| 200 | Leu | Glu | Arg | Asp | Val | Asp | Ile | Asn | Ile | Tyr | Asp | Trp | Asn | Gly | Gly | Thr |     |     |     |     |    |    |     |      |     |     |     |
| 201 |     |     |     |     |     |     |     |     |     | 180 |     |     |     |     |     |     |     | 185 |     |     |    |    |     |      |     | 190 |     |
| 203 | cca | ct  | g   | tc  | g   | c   | tt  | gt  | cc  | gg  | aa  | cc  | ac  | gt  | aa  | tt  | cg  | cc  | tt  | gg  | cc | cc | cc  | 1041 |     |     |     |
| 204 | Pro | Leu | Leu | Tyr | Ala | Val | Arg | Gly | Asn | His | Val | Lys | Cys | Val | Glu | Ala |     |     |     |     |    |    |     |      |     |     |     |
| 205 |     |     |     |     |     |     |     |     |     | 195 |     |     |     |     |     |     |     | 200 |     |     |    |    |     |      |     | 205 |     |
| 207 | tt  | tg  | ct  | g   | cc  | cc | cc | cc  | 1089 |     |     |     |
| 208 | Leu | Leu | Ala | Arg | Gly | Ala | Asp | Leu | Thr | Th  | ra  | Glu | Ala | Asp | Ser | Gly | Tyr |     |     |     |    |    |     |      |     |     |     |
| 209 |     |     |     |     |     |     |     |     |     | 210 |     |     |     |     |     |     |     | 215 |     |     |    |    |     |      |     | 220 |     |
| 211 | acc | cc  | at  | g   | ac  | ct  | gg  | cc  | gt  | cc  | gt  | cc  | g   | ta  | cc  | gg  | aa  | gt  | cc  | aa  | ca | cc | cc  | 1137 |     |     |     |
| 212 | Thr | Pro | Met | Asp | Leu | Ala | Val | Ala | Leu | Gly | Tyr | Arg | Lys | Val | Gln | Gln |     |     |     |     |    |    |     |      |     |     |     |
| 213 | 225 |     |     |     |     |     |     |     |     | 230 |     |     |     |     |     |     |     | 235 |     |     |    |    |     |      |     | 240 |     |
| 215 | gt  | at  | g   | ag  | aa  | c   | ac  | at  | ct  | aa  | gt  | cc  | tg  | cc  | tg  | cc  | cc  | cc  | cc  | cc  | cc | cc | cc  | 1185 |     |     |     |

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,243A

DATE: 10/29/2001

TIME: 13:29:31

Input Set : A:\B3991AB\_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

216 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro  
 217 245 250 255  
 219 gct gac cct gag tga agggcgctg ccggggactc agacactcag ggaacaaaat 1240  
 220 Ala Asp Pro Glu  
 221 260  
 223 ggtcagccag agctggggaa acccagaact gacttcaaag gcagcttctg gacaggtgg 1300  
 225 gggaggggac cttcccaag aggaaccaat aaaccttctg tgcag 1345  
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 229 <211> LENGTH: 260  
 230 <212> TYPE: PRT  
 231 <213> ORGANISM: Homo sapiens  
 233 <400> SEQUENCE: 11  
 234 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr  
 235 1 5 10 15  
 237 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala  
 238 20 25 30  
 240 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu  
 241 35 40 45  
 243 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly  
 244 50 55 60  
 246 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn  
 247 65 70 75 80  
 249 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln  
 250 85 90 95  
 252 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys  
 253 100 105 110  
 255 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu  
 256 115 120 125  
 258 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu  
 259 130 135 140  
 261 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala  
 262 145 150 155 160  
 264 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu  
 265 165 170 175  
 267 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr  
 268 180 185 190  
 270 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala  
 271 195 200 205  
 273 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr  
 274 210 215 220  
 276 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln  
 277 225 230 235 240  
 279 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro  
 280 245 250 255  
 282 Ala Asp Pro Glu  
 283 260  
 292 <210> SEQ ID NO: 12  
 293 <211> LENGTH: 260  
 294 <212> TYPE: PRT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,243A

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Input Set : A:\B3991AB\_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

295 <213> ORGANISM: Homo sapiens  
 297 <400> SEQUENCE: 12  
 298 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr  
 299 1 5 10 15  
 301 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala  
 302 20 25 30  
 304 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu  
 305 35 40 45  
 307 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly  
 308 50 55 60  
 310 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn  
 311 65 70 75 80  
 313 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln  
 314 85 90 95  
 316 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys  
 317 100 105 110  
 319 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu  
 320 115 120 125  
 322 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu  
 323 130 135 140  
 325 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala  
 326 145 150 155 160  
 328 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu  
 329 165 170 175  
 331 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr  
 332 180 185 190  
 334 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala  
 335 195 200 205  
 337 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr  
 338 210 215 220  
 340 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln  
 341 225 230 235 240  
 343 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro  
 344 245 250 255  
 346 Ala Asp Pro Glu  
 347 260  
 350 <210> SEQ ID NO: 13  
 351 <211> LENGTH: 269  
 352 <212> TYPE: PRT  
 353 <213> ORGANISM: Murinae gen. sp.  
 355 <400> SEQUENCE: 13  
 356 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro  
 357 1 5 10 15  
 359 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro  
 360 20 25 30  
 362 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp  
 363 35 40 45  
 365 Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser  
 366 50 55 60

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

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<210> SEQ ID NO 18  
<211> LENGTH: 220  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: UNSURE  
<222> LOCATION: 31  
<221> NAME/KEY: UNSURE  
<222> LOCATION: 148  
<221> NAME/KEY: UNSURE  
<222> LOCATION: 159  
<400> SEQUENCE: 18

12:30 pm 11/07/01

Sequence listing as of  
the above time and date.

Field 223 is required  
to enumerate unknown Xaa's  
and possible values

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/840,243A

DATE: 10/29/2001

TIME: 13:29:32

Input Set : A:\B3991AB\_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

L:496 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:18

L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:520 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:18

L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18